

**Amendments to the Sequence Listing:**

The attached sequence listing on sheets 1/13 – 13/13 is amended at heading line <110> to correctly identify the applicants. The sequences are not amended.

Attachment: Replacement sheets 1/13 to 13/13

1/13

## SEQUENCE LISTING

&lt;110&gt; Genesis Group Inc., Kenneth Kao, Catherine Popadiuk

&lt;120&gt; Pygopus in Diagnosis and Treatment of Cancer

&lt;130&gt; 50680-4

&lt;150&gt; US 60/463 309

&lt;151&gt; 2003-04-17

&lt;150&gt; US 60/496 012

&lt;151&gt; 2003-08-19

&lt;160&gt; 28

&lt;170&gt; PatentIn version 3.3

&lt;210&gt; 1

&lt;211&gt; 3190

&lt;212&gt; DNA

&lt;213&gt; homosapiens

&lt;220&gt;

&lt;223&gt; hPygo-2

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (173)..(1393)

<400> 1  
gtctggagag agcgcgcagt ttgcgcggcg gctcggcgct tccctgtcgt cgcactttgt 60  
ggttgctgca gctcgggggc ctgggctgcc cctgacaccc cttctgggcg atggtgcagc 120  
  
ccaagggcgc ctccatcccc cgccgctgcc gctaaccggg gtccccact cc atg gcc 178  
Met Ala  
1  
  
gcc tcg gcg ccg ccc cca ccg gac aag ctg gag gga ggt ggc ggc ccc 226  
Ala Ser Ala Pro Pro Pro Pro Asp Lys Leu Glu Gly Gly Gly Gly Pro  
5 10 15  
  
gca ccg ccc cct gcg ccg ccc agc acc ggg agg aag cag ggc aag gcc 274  
Ala Pro Pro Pro Ala Pro Pro Ser Thr Gly Arg Lys Gln Gly Lys Ala  
20 25 30  
  
ggt ctg caa atg aag agt cca gaa aag aag cga agg aag tca aat act 322  
Gly Leu Gln Met Lys Ser Pro Glu Lys Lys Arg Arg Lys Ser Asn Thr  
35 40 45 50  
  
cag ggc cct gca tac tca cat ctg acg gag ttt gca cca ccc cca act 370  
Gln Gly Pro Ala Tyr Ser His Leu Thr Glu Phe Ala Pro Pro Pro Thr  
55 60 65  
  
ccc atg gtg gat cac ctg gtt gca tcc aac cct ttt gaa gat gac ttc 418  
Pro Met Val Asp His Leu Val Ala Ser Asn Pro Phe Glu Asp Asp Phe  
70 75 80

gga gcc ccc aaa gtg ggg gtt gca gcc cct cca ttc ctt ggc agt cct Gly Ala Pro Lys Val Gly Val Ala Ala Pro Pro Phe Leu Gly Ser Pro 85 90 95	466
gtg ccc ttc gga ggc ttc cgt gtg cag ggg ggc atg gcg ggc cag gta Val Pro Phe Gly Gly Phe Arg Val Gln Gly Gly Met Ala Gly Gln Val 100 105 110	514
ccc cca ggc tac agc act gga ggt gga ggg ggc ccc cag cca ctc cgt Pro Pro Gly Tyr Ser Thr Gly Gly Gly Gly Gly Pro Gln Pro Leu Arg 115 120 125 130	562
cga cag cca ccc ccc ttc cct ccc aat cct atg ggc cct gct ttc aac Arg Gln Pro Pro Pro Phe Pro Pro Asn Pro Met Gly Pro Ala Phe Asn 135 140 145	610
atg ccc ccc cag ggt cct ggc tac cca ccc cca ggc aac atg aac ttt Met Pro Pro Gln Gly Pro Gly Tyr Pro Pro Pro Gly Asn Met Asn Phe 150 155 160	658
ccc agc caa ccc ttc aac cag cct ctg ggt caa aac ttt agt cct ccc Pro Ser Gln Pro Phe Asn Gln Pro Leu Gly Gln Asn Phe Ser Pro Pro 165 170 175	706
agt ggg cag atg atg ccg ggc cca gtg ggg gga ttt ggt ccc atg atc Ser Gly Gln Met Met Pro Gly Pro Val Gly Gly Phe Gly Pro Met Ile 180 185 190	754
tca ccc acc atg gga cag cct ccc aga gca gag ctg ggc cca cct tct Ser Pro Thr Met Gly Gln Pro Pro Arg Ala Glu Leu Gly Pro Pro Ser 195 200 205 210	802
ctg tcc caa cga ttt gct cag cca ggg gct cct ttt ggc cct tct cct Leu Ser Gln Arg Phe Ala Gln Pro Gly Ala Pro Phe Gly Pro Ser Pro 215 220 225	850
ctc cag aga cct ggt cag ggg ctc ccc agc ctg ccg cct aac aca agt Leu Gln Arg Pro Gly Gln Gly Leu Pro Ser Leu Pro Pro Asn Thr Ser 230 235 240	898
ccc ttt cct ggt ccg gac cct ggc ttt cct ggc cct ggt ggt gag gat Pro Phe Pro Gly Pro Asp Pro Gly Phe Pro Gly Pro Gly Gly Glu Asp 245 250 255	946
ggg ggg aag ccc ttg aat cca cct gct tct act gct ttt ccc cag gag Gly Gly Lys Pro Leu Asn Pro Pro Ala Ser Thr Ala Phe Pro Gln Glu 260 265 270	994
ccc cac tca ggc tcc ccg gct gct gct gtt aat ggg aac cag ccc agt Pro His Ser Gly Ser Pro Ala Ala Ala Val Asn Gly Asn Gln Pro Ser 275 280 285 290	1042
ttc ccc ccg aac agc agt ggg ccg ggt ggg ggc act cca gat gcc aac Phe Pro Pro Asn Ser Ser Gly Arg Gly Gly Gly Thr Pro Asp Ala Asn 295 300 305	1090
agc ttg gca ccc cct ggc aag gca ggt ggg ggc tcc ggg ccc cag cct Ser Leu Ala Pro Pro Gly Lys Ala Gly Gly Gly Ser Gly Pro Gln Pro 310 315 320	1138

```

ccc cca ggc ttg gtg tac cca tgt ggt gcc tgt cgg agt gag gtg aac      1186
Pro Pro Gly Leu Val Tyr Pro Cys Gly Ala Cys Arg Ser Glu Val Asn
      325              330              335

gat gac cag gat gcc att ctg tgt gag gcc tcc tgc cag aaa tgg ttc      1234
Asp Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys Trp Phe
      340              345              350

cac cgt gag tgc aca ggc atg act gag agc gcc tat ggg ctg ctg acc      1282
His Arg Glu Cys Thr Gly Met Thr Glu Ser Ala Tyr Gly Leu Leu Thr
      355              360              365              370

act gaa gct tct gcc gtc tgg gcc tgc gat ctc tgc ctc aag acc aag      1330
Thr Glu Ala Ser Ala Val Trp Ala Cys Asp Leu Cys Leu Lys Thr Lys
      375              380              385

gag atc cag tct gtc tac atc cgt gag ggc atg ggg cag ctg gtg gct      1378
Glu Ile Gln Ser Val Tyr Ile Arg Glu Gly Met Gly Gln Leu Val Ala
      390              395              400

gct aac gat ggg tga cgctggtgaa gtggcccagg gaagtgcaca tgtctctccc      1433
Ala Asn Asp Gly
      405

tgtctctcca ggggtgatttt tttgatgttt ggctcttggt ccttgtttcc actggctttc      1493
catcccatg gggcagaaac agtggctcct gggagcagaa aaggaattga ggtgggcagg      1553
cagaagagcc tggattgctc actgttttg gaaacttaca tgttgagatc tacagagatc      1613
caggaaacca aagccctgct gagcagagcc attttgtggc tatttctgga ggcccaggag      1673
tgtggctgca agagaaaagg ggctggagga agatccggag ggcaggggtg tccctctgc      1733
tgatgatgga tgcccctaac acctgtgcct aacacccta ctgaaccca cagctccagc      1793
cctagttttt ggagtcaagt gttaaagtt tctggccaga ggaattgggg tcttgccatc      1853
cctgcaatag cccctttatg ggctctggga gacagcttta gggaataaat ggggattttc      1913
ccctttttct acccactcct ttgcttcctc caagacttac ccaactcctt cccctcaga      1973
gaaccaaata gcctgaggaa gcaggagagt tcctggttat ggcagtttct tgggtgatttg      2033
gggcttcaag acagtaggtg agagatgctg tcaggacgta tcttcttcat accaaagtca      2093
ctggtccttt ctcagcctct ctcgtgcttt tctcctaata accatatttt tgccaaaaat      2153
tgggatatgt tatctgacag accagaatat ttgaagtttg ggctgtcctg aaagtctgga      2213
ctttggtggt accctcctcc cccagcccat ctgttgcaaa ttatactccg tgtgttcttc      2273
aactttcggc gcccttattc ccctgccttc ctggcttgat tgaaggaaag cttgaaaagg      2333
cgcagagccc tatacctcat ttctcccatg ataaaaggat ccaagtgagg ccctgtcaca      2393
gcctgtgggt aggggatgcg gcgggaccc cattgccatg gtactcaaag gtagaagagc      2453
ctggagtgtg ttgcttctct ttgctattct ttcatactct cttgggcctg gtgattaatt      2513
agcaattctc attcctctca gccaaaggcc tgcactgggc tttatttgct tttttttatt      2573
ttttaagcac tgccctgccag agatgggcct ggggcctgat gaggacctta gcgctgctcg      2633
ttctcctttt ctgttcatgc acacattcct ccattgggtg gggaaggcag gcatgggggtg      2693
tgccctcggc agaagttagg agtccccag ctcaagatac agtggcaaag acctagtgtg      2753
cccctacccc cacttctctc agttcctggc atgaggagag aagaccctgc tctggtggag      2813
ctgacaacct ttgaggctgg gaggagagca gcctctgggc atcgttccca gtgtccctca      2873
cactaaaacg gcgtagatgg caacccccca cccccacccc gctgctcaac tcttggtgtt      2933
gttggttctgt ttgccccatt tatctgttgc tgtttttgtg ttgtcttccc ctgctccgca      2993
ttttgtaaaa tggcccttgg gggagtgttt ttgctggatc tgctccctct cgctctctca      3053
ctccactact ttttggaaca agtgatggca gaatgcggtg gtggtggggg tcttttgtac      3113
tgttggatta ataaaatgat tttaaaatcc caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      3173
aaaaaaaaaa aaaaaaa
      3190

```

```

<210> 2
<211> 406
<212> PRT
<213> homosapiens

```

&lt;220&gt;

&lt;223&gt; hPygo-2

&lt;400&gt; 2

```

Met Ala Ala Ser Ala Pro Pro Pro Pro Asp Lys Leu Glu Gly Gly Gly
1          5          10          15

Gly Pro Ala Pro Pro Pro Ala Pro Pro Ser Thr Gly Arg Lys Gln Gly
20          25          30

Lys Ala Gly Leu Gln Met Lys Ser Pro Glu Lys Lys Arg Arg Lys Ser
35          40          45

Asn Thr Gln Gly Pro Ala Tyr Ser His Leu Thr Glu Phe Ala Pro Pro
50          55          60

Pro Thr Pro Met Val Asp His Leu Val Ala Ser Asn Pro Phe Glu Asp
65          70          75          80

Asp Phe Gly Ala Pro Lys Val Gly Val Ala Ala Pro Pro Phe Leu Gly
85          90          95

Ser Pro Val Pro Phe Gly Gly Phe Arg Val Gln Gly Gly Met Ala Gly
100         105         110

Gln Val Pro Pro Gly Tyr Ser Thr Gly Gly Gly Gly Gly Pro Gln Pro
115         120         125

Leu Arg Arg Gln Pro Pro Pro Phe Pro Pro Asn Pro Met Gly Pro Ala
130         135         140

Phe Asn Met Pro Pro Gln Gly Pro Gly Tyr Pro Pro Pro Gly Asn Met
145         150         155         160

Asn Phe Pro Ser Gln Pro Phe Asn Gln Pro Leu Gly Gln Asn Phe Ser
165         170         175

Pro Pro Ser Gly Gln Met Met Pro Gly Pro Val Gly Gly Phe Gly Pro
180         185         190

Met Ile Ser Pro Thr Met Gly Gln Pro Pro Arg Ala Glu Leu Gly Pro
195         200         205

Pro Ser Leu Ser Gln Arg Phe Ala Gln Pro Gly Ala Pro Phe Gly Pro
210         215         220

Ser Pro Leu Gln Arg Pro Gly Gln Gly Leu Pro Ser Leu Pro Pro Asn
225         230         235         240

Thr Ser Pro Phe Pro Gly Pro Asp Pro Gly Phe Pro Gly Pro Gly Gly
245         250         255

Glu Asp Gly Gly Lys Pro Leu Asn Pro Pro Ala Ser Thr Ala Phe Pro
260         265         270

Gln Glu Pro His Ser Gly Ser Pro Ala Ala Ala Val Asn Gly Asn Gln
275         280         285

Pro Ser Phe Pro Pro Asn Ser Ser Gly Arg Gly Gly Gly Thr Pro Asp
290         295         300

```

Ala Asn Ser Leu Ala Pro Pro Gly Lys Ala Gly Gly Gly Ser Gly Pro  
 305 310 315 320

Gln Pro Pro Pro Gly Leu Val Tyr Pro Cys Gly Ala Cys Arg Ser Glu  
 325 330 335

Val Asn Asp Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys  
 340 345 350

Trp Phe His Arg Glu Cys Thr Gly Met Thr Glu Ser Ala Tyr Gly Leu  
 355 360 365

Leu Thr Thr Glu Ala Ser Ala Val Trp Ala Cys Asp Leu Cys Leu Lys  
 370 375 380

Thr Lys Glu Ile Gln Ser Val Tyr Ile Arg Glu Gly Met Gly Gln Leu  
 385 390 395 400

Val Ala Ala Asn Asp Gly  
 405

<210> 3  
 <211> 1260  
 <212> DNA  
 <213> homosapiens

<220>  
 <221> CDS  
 <222> (1)..(1260)

<220>  
 <223> hPygo-1

<400> 3  
 atg ccc gcc gag aac tct cca gct ccc gct tac aaa gtt tcc tcg cat 48  
 Met Pro Ala Glu Asn Ser Pro Ala Pro Ala Tyr Lys Val Ser Ser His  
 1 5 10 15

ggt ggt gat agt gga ctg gat ggg tta gga gga cca ggt gta caa cta 96  
 Gly Gly Asp Ser Gly Leu Asp Gly Leu Gly Gly Pro Gly Val Gln Leu  
 20 25 30

gga agc cca gat aag aaa aag cgc aag gca aat aca cag gga cct tct 144  
 Gly Ser Pro Asp Lys Lys Lys Arg Lys Ala Asn Thr Gln Gly Pro Ser  
 35 40 45

ttc cct cca ttg tct gag tat gct cca cca ccg aat cca aac tct gac 192  
 Phe Pro Pro Leu Ser Glu Tyr Ala Pro Pro Pro Asn Pro Asn Ser Asp  
 50 55 60

cat cta gtg gct gct aat cca ttt gat gac aac tat aat act att tcc 240  
 His Leu Val Ala Ala Asn Pro Phe Asp Asp Asn Tyr Asn Thr Ile Ser  
 65 70 75 80

tat aaa cca cta cct tcg tca aat cca tat ctt ggc cct ggt tat cct 288  
 Tyr Lys Pro Leu Pro Ser Ser Asn Pro Tyr Leu Gly Pro Gly Tyr Pro  
 85 90 95

ggc ttt gga ggc tat agt aca ttc aga atg cca cct cac gtt ccc cca Gly Phe Gly Gly Tyr Ser Thr Phe Arg Met Pro Pro His Val Pro Pro 100 105 110	336
aga atg tct tcc cca tac tgt ggt cct tac tca ctc agg aac cag cca Arg Met Ser Ser Pro Tyr Cys Gly Pro Tyr Ser Leu Arg Asn Gln Pro 115 120 125	384
cac cca ttt cct cag aat cct ctg ggc atg ggt ttt aat cga cct cat His Pro Phe Pro Gln Asn Pro Leu Gly Met Gly Phe Asn Arg Pro His 130 135 140	432
gct ttt aac ttt ggg cca cat gat aat tca agt ttc ggt aat cca tct Ala Phe Asn Phe Gly Pro His Asp Asn Ser Ser Phe Gly Asn Pro Ser 145 150 155 160	480
tat aat aat gca cta agt cag aat gtc aac atg cct aat caa cat ttt Tyr Asn Asn Ala Leu Ser Gln Asn Val Asn Met Pro Asn Gln His Phe 165 170 175	528
aga caa aat cct gct gaa aat ttc agt caa att cct cca cag aat gct Arg Gln Asn Pro Ala Glu Asn Phe Ser Gln Ile Pro Pro Gln Asn Ala 180 185 190	576
agc caa gtt tct aac ccc gat ttg gca tct aat ttt gtt cct gga aat Ser Gln Val Ser Asn Pro Asp Leu Ala Ser Asn Phe Val Pro Gly Asn 195 200 205	624
aat tca aat ttt act tct ccg tta gaa tct aat cat tct ttt att cct Asn Ser Asn Phe Thr Ser Pro Leu Glu Ser Asn His Ser Phe Ile Pro 210 215 220	672
ccc cca aac act ttt ggt caa gca aaa gca cca ccc cca aaa caa gac Pro Pro Asn Thr Phe Gly Gln Ala Lys Ala Pro Pro Pro Lys Gln Asp 225 230 235 240	720
ttt act caa gga gca acc aaa aac act aat caa aat tcc tct gct cat Phe Thr Gln Gly Ala Thr Lys Asn Thr Asn Gln Asn Ser Ser Ala His 245 250 255	768
cca cct cac ttg aat atg gat gac aca gtg aat cag agt aat att gaa Pro Pro His Leu Asn Met Asp Asp Thr Val Asn Gln Ser Asn Ile Glu 260 265 270	816
tta aaa aat gtt aat cga aac aat gca gta aat cag gag aac agc cgt Leu Lys Asn Val Asn Arg Asn Asn Ala Val Asn Gln Glu Asn Ser Arg 275 280 285	864
tca agt agc act gaa gcc aca aac aat aac cct gca aat ggg acg cag Ser Ser Ser Thr Glu Ala Thr Asn Asn Asn Pro Ala Asn Gly Thr Gln 290 295 300	912
aat aag cca cga caa cca aga ggt gca gca gat gcc tgc acc aca gaa Asn Lys Pro Arg Gln Pro Arg Gly Ala Ala Asp Ala Cys Thr Thr Glu 305 310 315 320	960
aaa agc aat aaa tcc tct ctt cac cca aac cgt cat ggc cat tcg tct Lys Ser Asn Lys Ser Ser Leu His Pro Asn Arg His Gly His Ser Ser 325 330 335	1008

tct gac cca gtg tat cct tgt gga att tgt aca aac gag gtg aac gat	1056
Ser Asp Pro Val Tyr Pro Cys Gly Ile Cys Thr Asn Glu Val Asn Asp	
340 345 350	
gat cag gat gcc atc tta tgt gag gcc tct tgt cag aaa tgg ttt cat	1104
Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys Trp Phe His	
355 360 365	
cgg atc tgt act gga atg act gaa aca gct tat ggc ctc tta act gca	1152
Arg Ile Cys Thr Gly Met Thr Glu Thr Ala Tyr Gly Leu Leu Thr Ala	
370 375 380	
gaa gca tct gca gta tgg ggc tgt gat acc tgt atg gct gac aaa gat	1200
Glu Ala Ser Ala Val Trp Gly Cys Asp Thr Cys Met Ala Asp Lys Asp	
385 390 395 400	
gtc cag tta atg cgt act aga gaa act ttt ggt cca tct gca gtg ggc	1248
Val Gln Leu Met Arg Thr Arg Glu Thr Phe Gly Pro Ser Ala Val Gly	
405 410 415	
agt gat gct taa	1260
Ser Asp Ala	

<210> 4  
 <211> 419  
 <212> PRT  
 <213> homosapiens

<220>  
 <223> hPygo-1

<400> 4  
 Met Pro Ala Glu Asn Ser Pro Ala Pro Ala Tyr Lys Val Ser Ser His  
 1 5 10 15  
 Gly Gly Asp Ser Gly Leu Asp Gly Leu Gly Gly Pro Gly Val Gln Leu  
 20 25 30  
 Gly Ser Pro Asp Lys Lys Lys Arg Lys Ala Asn Thr Gln Gly Pro Ser  
 35 40 45  
 Phe Pro Pro Leu Ser Glu Tyr Ala Pro Pro Pro Asn Pro Asn Ser Asp  
 50 55 60  
 His Leu Val Ala Ala Asn Pro Phe Asp Asp Asn Tyr Asn Thr Ile Ser  
 65 70 75 80  
 Tyr Lys Pro Leu Pro Ser Ser Asn Pro Tyr Leu Gly Pro Gly Tyr Pro  
 85 90 95  
 Gly Phe Gly Gly Tyr Ser Thr Phe Arg Met Pro Pro His Val Pro Pro  
 100 105 110  
 Arg Met Ser Ser Pro Tyr Cys Gly Pro Tyr Ser Leu Arg Asn Gln Pro  
 115 120 125  
 His Pro Phe Pro Gln Asn Pro Leu Gly Met Gly Phe Asn Arg Pro His  
 130 135 140



Ala Phe Asn Phe Gly Pro His Asp Asn Ser Ser Phe Gly Asn Pro Ser  
 145 150 155 160  
 Tyr Asn Asn Ala Leu Ser Gln Asn Val Asn Met Pro Asn Gln His Phe  
 165 170 175  
 Arg Gln Asn Pro Ala Glu Asn Phe Ser Gln Ile Pro Pro Gln Asn Ala  
 180 185 190  
 Ser Gln Val Ser Asn Pro Asp Leu Ala Ser Asn Phe Val Pro Gly Asn  
 195 200 205  
 Asn Ser Asn Phe Thr Ser Pro Leu Glu Ser Asn His Ser Phe Ile Pro  
 210 215 220  
 Pro Pro Asn Thr Phe Gly Gln Ala Lys Ala Pro Pro Pro Lys Gln Asp  
 225 230 235 240  
 Phe Thr Gln Gly Ala Thr Lys Asn Thr Asn Gln Asn Ser Ser Ala His  
 245 250 255  
 Pro Pro His Leu Asn Met Asp Asp Thr Val Asn Gln Ser Asn Ile Glu  
 260 265 270  
 Leu Lys Asn Val Asn Arg Asn Asn Ala Val Asn Gln Glu Asn Ser Arg  
 275 280 285  
 Ser Ser Ser Thr Glu Ala Thr Asn Asn Asn Pro Ala Asn Gly Thr Gln  
 290 295 300  
 Asn Lys Pro Arg Gln Pro Arg Gly Ala Ala Asp Ala Cys Thr Thr Glu  
 305 310 315 320  
 Lys Ser Asn Lys Ser Ser Leu His Pro Asn Arg His Gly His Ser Ser  
 325 330 335  
 Ser Asp Pro Val Tyr Pro Cys Gly Ile Cys Thr Asn Glu Val Asn Asp  
 340 345 350  
 Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys Trp Phe His  
 355 360 365  
 Arg Ile Cys Thr Gly Met Thr Glu Thr Ala Tyr Gly Leu Leu Thr Ala  
 370 375 380  
 Glu Ala Ser Ala Val Trp Gly Cys Asp Thr Cys Met Ala Asp Lys Asp  
 385 390 395 400  
 Val Gln Leu Met Arg Thr Arg Glu Thr Phe Gly Pro Ser Ala Val Gly  
 405 410 415

Ser Asp Ala

<210> 5  
 <211> 20  
 <212> DNA  
 <213> artificial  
  
 <220>  
 <223> HpyI antisense ON

<400> 5  
gagctgcagc aaccacaaag

20

<210> 6  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> Hpy2 antisense ON

<400> 6  
ggacccgggt tagcggcagc g

21

<210> 7  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> Hpy3 antisense ON

<400> 7  
ccacctccct ccagcttgtc c

21

<210> 8  
<211> 19  
<212> DNA  
<213> artificial

<220>  
<223> Hpy4 antisense ON

<400> 8  
ggaggactaa agttttgac

19

<210> 9  
<211> 19  
<212> DNA  
<213> artificial

<220>  
<223> Hpy5 antisense ON

<400> 9  
ggctgagcaa atcgttggg

19

<210> 10  
<211> 20  
<212> DNA  
<213> artificial

<220>  
<223> Hpy6 antisense ON

<400> 10  
gaaaagcagt agaagcagg

20

<210> 11  
<211> 18  
<212> DNA  
<213> artificial

<220>  
<223> Hpy7 antisense ON

<400> 11  
ctcacggatg tagacaga

18

<210> 12  
<211> 19  
<212> DNA  
<213> artificial

<220>  
<223> Hpy8 antisense ON

<400> 12  
cctctggcca gaaaccttt

19

<210> 13  
<211> 19  
<212> DNA  
<213> artificial

<220>  
<223> Hpy9 antisense ON

<400> 13  
ctcttctacc tttgagtac

19

<210> 14  
<211> 18  
<212> DNA  
<213> artificial

<220>  
<223> Hpy10 antisense ON

<400> 14  
cactgtatct tgagctgg

18

<210> 15  
<211> 19  
<212> RNA  
<213> artificial

<220>  
<223> Hpy2A siRNA

<400> 15  
cgaugaccag gaugccauu 19

<210> 16  
<211> 19  
<212> RNA  
<213> artificial

<220>  
<223> Hpy2B siRNA

<400> 16  
agaagcgaag gaagucaaa 19

<210> 17  
<211> 19  
<212> RNA  
<213> artificial

<220>  
<223> Hpy2C siRNA

<400> 17  
ugggaaccag cccaguuuc 19

<210> 18  
<211> 19  
<212> RNA  
<213> artificial

<220>  
<223> Hpy2D siRNA

<400> 18  
ccagccucug ggucaaaaac 19

<210> 19  
<211> 19  
<212> RNA  
<213> artificial

<220>  
<223> Hpy2E siRNA

<400> 19  
cuuucccagc caaccuuuc 19

<210> 20  
<211> 19  
<212> DNA  
<213> artificial

<220>  
<223> mismatched sequence to Hpy5

<400> 20  
gcctgagcta atcattggt 19

<210> 21  
<211> 18  
<212> DNA  
<213> artificial

<220>  
<223> anti-Xenopus pygo2

<400> 21  
tttgcccggt ttcttctc 18

<210> 22  
<211> 24  
<212> DNA  
<213> artificial

<220>  
<223> Forward hPygo2 primer

<400> 22  
gcatccaacc cttttgaaga tgac 24

<210> 23  
<211> 25  
<212> DNA  
<213> artificial

<220>  
<223> Reverse hPygo2 primer

<400> 23  
tcagccaggg ggtgccaaagc tgttg 25

<210> 24  
<211> 20  
<212> DNA  
<213> artificial

<220>  
<223> Forward hPygo1 primer

<400> 24  
gccacgacaa ccaagagggtg 20

<210> 25  
<211> 22  
<212> DNA  
<213> artificial

<220>  
<223> Reverse hPygo1 primer

<400> 25  
ccagtacaga tccgatgaaa cc 22

<210> 26  
<211> 20  
<212> DNA  
<213> artificial

<220>  
<223> Forward Bcl-9 primer

<400> 26  
gatgttgtcc tgggtgtcttg 20

<210> 27  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> Reverse Bcl-9 primer

<400> 27  
ggtcacgaca ctgcagtgct c 21

<210> 28  
<211> 19  
<212> DNA  
<213> artificial

<220>  
<223> mismatched sequence to Hpy5

<400> 28  
gtctgagcta atcattggt 19